

SEQUENCE LISTING

<110> Valladeau, Jenny
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Ford, John
Lebecque, Serge J.E.
Saeland, Sem

<120> Isolated Mammalian Membrane Protein Genes; Related Reagents

<130> SF0695 B

<140> US 09/862,802
<141> 2001-05-22

<150> US 60/053,080
<151> 1997-07-09

<150> US 09/111,470
<151> 1998-07-08

<160> 13

<170> PatentIn version 3.1

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ctccactagt tgagtgaaag gaaggaggta atttaccacc atgtttggtt cctgtttata 180
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t atg act tcg gaa atc act tat gct gaa gtg agg ttc aaa aat gaa ttc 289
Met Thr Ser Glu Ile Thr Tyr Ala Glu Val Arg Phe Lys Asn Glu Phe
1 5 10 15

aag tcc tca ggc atc aac aca gcc tct tct gca gct tcc aag gag agg 337
Lys Ser Ser Gly Ile Asn Thr Ala Ser Ser Ala Ala Ser Lys Glu Arg
20 25 30

act gcc cct ctc aaa agt aat acc gga ttc ccc aag ctg ctt tgt gcc 385
Thr Ala Pro Leu Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala
35 40 45

tca ctg ttg ata ttt ttc ctg cta ttg gca atc tca ttc ttt att gct Ser Leu Leu Ile Phe Phe Leu Leu Leu Ala Ile Ser Phe Phe Ile Ala 50 55 60	433
ttt gtc att ttc ttt caa aaa tat tct cag ctt ctt gaa aaa aag act Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr 65 70 75 80	481
aca aaa gag ctg gtt cat aca aca ttg gag tgt gtg aaa aaa aat atg Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met 85 90 95	529
ccc gtg gaa gag aca gcc tgg agc tgt tgc cca aag aat tgg aag tca Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser 100 105 110	577
ttt agt tcc aac tgc tac ttt att tct act gaa tca gca tct tgg caa Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln 115 120 125	625
gac agt gag aag gac tgt gct aga atg gag gct cac ctg ctg gtg ata Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile 130 135 140	673
aac act caa gaa gag cag gat ttc atc ttc cag aat ctg caa gaa gaa Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu 145 150 155 160	721
tct gct tat ttt gtg ggg ctc tca gat cca gaa ggt cag cga cat tgg Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp 165 170 175	769
caa tgg gtt gat cag aca cca tac aat gaa agt tcc aca ttc tgg cat Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His 180 185 190	817
cca cgt gag ccc agt gat ccc aat gag cgc tgc gtt gtg cta aat ttt Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe 195 200 205	865
cgt aaa tca ccc aaa aga tgg ggc tgg aat gat gtt aat tgt ctt ggt Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly 210 215 220	913
cct caa agg tca gtt tgt gag atg atg aag atc cac tta tgaactgaac Pro Gln Arg Ser Val Cys Glu Met Met Lys Ile His Leu 225 230 235	962
attctccatg aacaggtgg tggattggta tctgtcattg tagggataga taataagctc	1022
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Thr Ala Pro Leu Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala
35 40 45

Ser Leu Leu Ile Phe Phe Leu Leu Leu Ala Ile Ser Phe Phe Ile Ala
50 55 60

Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr
65 70 75 80

Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met
85 90 95

Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser
100 105 110

Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln
115 120 125

Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile
130 135 140

Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu
145 150 155 160

Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp
165 170 175

Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His
180 185 190

Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe
195 200 205

Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly
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Pro Gln Arg Ser Val Cys Glu Met Met Lys Ile His Leu
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 <223> short form lacks nucleotides 608-673

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 <222> (775)..(776)
 <223> ASGPRm (Table 2) has sequence insert encoding GEE between nucleotides 775-776

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 <223> nucleotide 1064 of DCMP2s may be A, which would encode Asn rather than Asp at the residue numbered 270

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 gtcccacctc tggcccttgc agcacaacca acgtggaaat cacaccctcc agacctccca 180
 cagctccacc ccagactggg cgccggccct gcctccattt cagctgtgac aacctcagag 240
 ccgtgttggc ccaagc atg aca agg acg tat gaa aac ttc cag tac ttg gag 292
 Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu
 1 5 10

aat aag gtg aaa gtc cag ggg ttt aaa aat ggg cca ctt cct ctc cag 340
 Asn Lys Val Lys Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln
 15 20 25

tcc ctc ctg cag cgt ctc cgc tct ggg ccc tgc cat ctc ctg ctg tcc 388
 Ser Leu Leu Gln Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser
 30 35 40

ctg ggc ctc ggc ctg ctg ctg gtc atc atc tgt gtg gtt gga ttc Leu Gly Leu Gly Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe 45 50 55 60	436
caa aat tcc aaa ttt cag agg gac ctg gtg acc ctg aga aca gat ttt Gln Asn Ser Lys Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe 65 70 75	484
agc aac ttc acc tca aac act gtg gcg gag atc cag gca ctg act tcc Ser Asn Phe Thr Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser 80 85 90	532
cag ggc agc agc ttg gaa gaa acg ata gca tct ctg aaa gct gag gtg Gln Gly Ser Ser Leu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val 95 100 105	580
gag ggt ttc aag cag gaa cgg cag gca ggg gta tct gag ctc cag gaa Glu Gly Phe Lys Gln Glu Arg Gln Ala Gly Val Ser Glu Leu Gln Glu 110 115 120	628
cac act acg cag aag gca cac cta ggc cac tgt ccc cac tgc cca tct His Thr Thr Gln Lys Ala His Leu Gly His Cys Pro His Cys Pro Ser 125 130 135 140	676
gtg tgt gtc cca gtt cat tct gaa atg ctc ctg cga gtc cag cag ctg Val Cys Val Pro Val His Ser Glu Met Leu Leu Arg Val Gln Gln Leu 145 150 155	724
gtg caa gac ctg aag aaa ctg acc tgc cag gtg gct act ctc aac aac Val Gln Asp Leu Lys Leu Thr Cys Gln Val Ala Thr Leu Asn Asn 160 165 170	772
aat gcc tcc act gaa ggg acc tgc tgc ccc gtc aac tgg gtg gag cac Asn Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu His 175 180 185	820
caa gac agc tgc tac tgg ttc tct cac tct ggg atg tcc tgg gcc gag Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala Glu 190 195 200	868
gct gag aag tac tgc cag ctg aag aac gcc cac ctg gtg gtc atc aac Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile Asn 205 210 215 220	916
tcc agg gag gag cag aat ttt gtc cag aaa tat cta ggc tcc gca tac Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala Tyr 225 230 235	964
acc tgg atg ggc ctc agt gac cct gaa gga gcc tgg aag tgg gtg gat Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val Asp 240 245 250	1012
gga aca gac tat gcg acc ggc ttc cag aac tgg aag cca ggc cag cca Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln Pro 255 260 265	1060
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ttc cat cca gac ggc agg tgg aat gac gac gtc tgc cag agg ccc tac Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr 285 290 295 300	1156
cac tgg gtc tgc gag gct ggc ctg ggt cag acc agc cag gag agt cac His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser His 305 310 315	1204
tgagctgcct ttgggtggac caccggcca cagaaatggc ggtgggagga ggactcttct cacgacacctcc tcgcaagacc gctctggag agaaaataagc actgggagat tggaagcact gctaacattt tgaatttttt tctcttaat tttaaaaaga tggatatgtg ttcttaagct tttatttttt ttccaacttt tgaaagtcaa cttcatgaag gtataatttt tacataataa aaatgcactc.attt	1264 1324 1384 1444 1458

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Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln
 20 25 30

Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly
 35 40 45

Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys

7

50	55	60
Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr		
65	70	75
Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser		
85	90	95
Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys		
100	105	110
Gln Glu Arg Gln Ala Gly Val Ser Glu Leu Gln Glu His Thr Thr Gln		
115	120	125
Lys Ala His Leu Gly His Cys Pro His Cys Pro Ser Val Cys Val Pro		
130	135	140
Val His Ser Glu Met Leu Leu Arg Val Gln Gln Leu Val Gln Asp Leu		
145	150	155
160		
Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn Asn Asn Ala Ser Thr		
165	170	175
Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu His Gln Asp Ser Cys		
180	185	190
Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala Glu Ala Glu Lys Tyr		
195	200	205
Cys Gln Leu Lys Asn Ala His Leu Val Val Ile Asn Ser Arg Glu Glu		
210	215	220
Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala Tyr Thr Trp Met Gly		
225	230	235
240		
Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val Asp Gly Thr Asp Tyr		
245	250	255
Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln Pro Asp Asp Trp Gln		
260	265	270
Gly His Gly Leu Gly Gly Glu Asp Cys Ala His Phe His Pro Asp		
275	280	285
Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr His Trp Val Cys		

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295

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Gln Arg Leu Cys Ser Gly Pro Arg Leu Leu Leu Ser Leu Gly Leu
35 40 45

Ser Leu Leu Leu Leu Val Val Val Cys Val Ile Gly Ser Gln Asn Ser
50 55 60

Gln Leu Gln Glu Glu Leu Arg Gly Leu Arg Glu Thr Phe Ser Asn Phe
65 70 75 80

Thr Ala Ser Thr Glu Ala Gln Val Lys Gly Leu Ser Thr Gln Gly Gly
85 90 95

Asn Val Gly Arg Lys Met Lys Ser Leu Glu Ser Gln Leu Glu Lys Gln
100 105 110

Gln Lys Asp Leu Ser Glu Asp His Ser Ser Leu Leu Leu His Val Lys
115 120 125

Gln Phe Val Ser Asp Leu Arg Ser Leu Ser Cys Gln Met Ala Ala Leu
130 135 140

Gln Gly Asn Gly Ser Glu Arg Thr Cys Cys Pro Val Asn Trp Val Glu
145 150 155 160

His Glu Arg Ser Cys Tyr Trp Phe Ser Arg Ser Gly Lys Ala Trp Ala
165 170 175

Asp Ala Asp Asn Tyr Cys Arg Leu Glu Asp Ala His Leu Val Val Val
 180 185 190

Thr Ser Trp Glu Glu Gln Lys Phe Val Gln His His Ile Gly Pro Val
 195 200 205

Asn Thr Trp Met Gly Leu His Asp Gln Asn Gly Pro Trp Lys Trp Val
 210 215 220

Asp Gly Thr Asp Tyr Glu Thr Gly Phe Lys Asn Trp Arg Pro Glu Gln
 225 230 235 240

Pro Asp Asp Trp Tyr Gly His Gly Leu Gly Gly Glu Asp Cys Ala
 245 250 255

His Phe Thr Asp Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro
 260 265 270

Tyr Arg Trp Val Cys Glu Thr Glu Leu Asp Lys Ala Ser Gln Glu Pro
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Pro Leu Leu
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Arg Leu Cys Ser Met Val Cys Phe Ser Leu Leu Ala Leu Ser Phe Asn
 35 40 45

Ile Leu Leu Leu Val Val Ile Cys Val Thr Gly Ser Gln Ser Ala Gln
 50 55 60

Leu Gln Ala Glu Leu Arg Ser Leu Lys Glu Ala Phe Ser Asn Phe Ser

10
65 70 75 80

Ser Ser Thr Leu Thr Glu Val Gln Ala Ile Ser Thr His Gly Gly Ser
85 90 95

Val Gly Asp Lys Ile Thr Ser Leu Gly Ala Lys Leu Glu Lys Gln Gln
100 105 110

Gln Asp Leu Lys Ala Asp His Asp Ala Leu Leu Phe His Leu Lys His
115 120 125

Phe Pro Val Asp Leu Arg Phe Val Ala Cys Gln Met Glu Leu Leu His
130 135 140

Ser Asn Gly Ser Gln Arg Thr Cys Cys Pro Val Asn Trp Val Glu His
145 150 155 160

Gln Gly Ser Cys Tyr Trp Phe Ser His Ser Gly Lys Ala Trp Ala Glu
165 170 175

Ala Glu Lys Tyr Cys Gln Leu Glu Asn Ala His Leu Val Val Ile Asn
180 185 190

Ser Trp Glu Glu Gln Lys Phe Ile Val Gln His Thr Asn Pro Phe Asn
195 200 205

Thr Trp Ile Gly Leu Thr Asp Ser Asp Gly Ser Trp Lys Trp Val Asp
210 215 220

Gly Thr Asp Tyr Arg His Asn Tyr Lys Asn Trp Ala Val Thr Gln Pro
225 230 235 240

Asp Asn Trp His Gly His Glu Leu Gly Gly Ser Glu Asp Cys Val Glu
245 250 255

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gtttCTTGTt ctcatctcgT ttatcctagt gagacatgtc tcttCTTCA tacaactgtg      180
caatatgaca acttatacaca gtgattggTT ctcataact atagagcTT agagaaggaa      240
caaggctctc ttctgacgga ggaagatTT ttcttgat atg gct tca gaa atc act      296
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                                         1           5

tat gca gaa gTG aag tTC aag aAT gaa tCC aAC tCC ttG cac acc tac      344
Tyr Ala Glu Val Lys Phe Lys Asn Glu Ser Asn Ser Leu His Thr Tyr
   10          15          20

tca gaa tct cct gca gct ccc aga gag aaa cct atc cgt gat cta aga      392
Ser Glu Ser Pro Ala Ala Pro Arg Glu Lys Pro Ile Arg Asp Leu Arg
   25          30          35

aag cct ggt tcc ccc tca ctg ctt aca tcc ctg atg cta ctt ctc      440
Lys Pro Gly Ser Pro Ser Leu Leu Leu Thr Ser Leu Met Leu Leu Leu
   40          45          50

ctg ctg ctg gca atc aca ttc tta gtt gct ttt atc att tat ttt caa      488
Leu Leu Leu Ala Ile Thr Phe Leu Val Ala Phe Ile Ile Tyr Phe Gln
   55          60          65          70

aag tac tctcaa ctt ctt gaa gaa aaa aaa gct gca aaa aat ata atg      536
Lys Tyr Ser Gln Leu Leu Glu Glu Lys Lys Ala Ala Lys Asn Ile Met
   75          80          85

cac aat gaa ttg aac tgc aca aaa agt gtt tca ccc atg gaa gac aaa      584
His Asn Glu Leu Asn Cys Thr Lys Ser Val Ser Pro Met Glu Asp Lys
   90          95          100

gtc tgg agc tgt tgc cca aag gat tgg agg cta ttt ggt tcc cac tgc      632
Val Trp Ser Cys Cys Pro Lys Asp Trp Arg Leu Phe Gly Ser His Cys
   105         110         115

tac ttg gtt ccc aca gtt tct tca tca gca tct tgg aac aag agt gag      680
Tyr Leu Val Pro Thr Val Ser Ser Ser Ala Ser Trp Asn Lys Ser Glu
   120         125         130

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12

gag aac tgc tcc cgc atg ggt gct cat cta gtg gtg atc caa agc cag Glu Asn Cys Ser Arg Met Gly Ala His Leu Val Val Ile Gln Ser Gln 135 140 145 150	728
gaa gag cag gat ttc atc act ggg atc ttg gac act cat gct gct tat Glu Glu Gln Asp Phe Ile Thr Gly Ile Leu Asp Thr His Ala Ala Tyr 155 160 165	776
ttt ata ggg ttg tgg gat aca ggc cat cgg caa tgg caa tgg gtt gat Phe Ile Gly Leu Trp Asp Thr Gly His Arg Gln Trp Gln Trp Val Asp 170 175 180	824
cag aca cca tat gaa gaa agt atc aca ttc tgg cac aat ggt gag ccc Gln Thr Pro Tyr Glu Ser Ile Thr Phe Trp His Asn Gly Glu Pro 185 190 195	872
agc agt ggc aat gaa aaa tgt gct aca ata att tac cgt tgg aag act Ser Ser Gly Asn Glu Lys Cys Ala Thr Ile Ile Tyr Arg Trp Lys Thr 200 205 210	920
gga tgg ggc tgg aac gat atc tct tgc agt ctt aaa cag aag tca gtt Gly Trp Gly Trp Asn Asp Ile Ser Cys Ser Leu Lys Gln Lys Ser Val 215 220 225 230	968
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tcattgttat ccaaccatta cacagacacc tggaaaattc tacaggttca cagaatttaa gtgggcagca aatggttatg catacactgg cccacatata tccttgca tttacccacc tactctgtca taaaatgaac tttcatttag aattttctat ataccacaga gtatacagag tcccttatgg acacacatgg aacttttgc catctgttt actcatgcca ttgtatgata ggttctcttg acctatctgt ttctgtttct ctgttgttt ttaatgtct tggtatgtt tgacattaaa ttgagaagta aaattataaa tatttaagtg tctggattga tacacacaga tatgtactat gaaatataat taaatattta ctgtcc	1082 1142 1202 1262 1322 1382 1418

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35 40 45

Ser Leu Met Leu Leu Leu Leu Leu Ala Ile Thr Phe Leu Val Ala
50 55 60

Phe Ile Ile Tyr Phe Gln Lys Tyr Ser Gln Leu Leu Glu Glu Lys Lys
65 70 75 80

Ala Ala Lys Asn Ile Met His Asn Glu Leu Asn Cys Thr Lys Ser Val
85 90 95

Ser Pro Met Glu Asp Lys Val Trp Ser Cys Cys Pro Lys Asp Trp Arg
100 105 110

Leu Phe Gly Ser His Cys Tyr Leu Val Pro Thr Val Ser Ser Ser Ala
115 120 125

Ser Trp Asn Lys Ser Glu Glu Asn Cys Ser Arg Met Gly Ala His Leu
130 135 140

Val Val Ile Gln Ser Gln Glu Glu Gln Asp Phe Ile Thr Gly Ile Leu
145 150 155 160

Asp Thr His Ala Ala Tyr Phe Ile Gly Leu Trp Asp Thr Gly His Arg
165 170 175

Gln Trp Gln Trp Val Asp Gln Thr Pro Tyr Glu Glu Ser Ile Thr Phe
180 185 190

Trp His Asn Gly Glu Pro Ser Ser Gly Asn Glu Lys Cys Ala Thr Ile
195 200 205

Ile Tyr Arg Trp Lys Thr Gly Trp Gly Trp Asn Asp Ile Ser Cys Ser
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Leu Lys Gln Lys Ser Val Cys Gln Met Lys Lys Ile Asn Leu
225 230 235

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cccaactctg agtgacgtcc cacctctggc cttgcagca caaccaacgt ggaaatcaca      120
ccctccagac ctccccacagg tccacccca actgggcgcc ggccctgcct ccatttcagc      180
tgtgacaacc tcagagccgt gttggcccaa gc atg aca agg acg tat gaa aac      240
                                         Met Thr Arg Thr Tyr Glu Asn
                                         1                      5
ttc cag tac ttg gag aat aag gtg aaa gtc cag ggg ttt aaa aat ggg      293
Phe Gln Tyr Leu Glu Asn Lys Val Lys Val Gln Gly Phe Lys Asn Gly
10          15          20
cca ctt cct ctc cag tcc ctc ctg ctg gtc atc atc tgt gtg gtt      341
Pro Leu Pro Leu Gln Ser Leu Leu Leu Val Ile Ile Cys Val Val
25          30          35
gga ttc caa aat tcc aaa ttt cag agg gac ctg gtg acc ctg aga aca      389
Gly Phe Gln Asn Ser Lys Phe Gln Arg Asp Leu Val Thr Leu Arg Thr
40          45          50          55
gat ttt agc aac ttc acc tca aac act gtg gcg gag atc cag gca ctg      437
Asp Phe Ser Asn Phe Thr Ser Asn Thr Val Ala Glu Ile Gln Ala Leu
60          65          70
act tcc cag ggc agc agc ttg gaa gaa acg ata gca tct ctg aaa gct      485
Thr Ser Gln Gly Ser Ser Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala
75          80          85
tag gtg gag ggt ttc aag cag gaa cg gca gtt cat tct gaa atg      533
Glu Val Glu Gly Phe Lys Gln Glu Arg Gln Ala Val His Ser Glu Met
90          95          100
tc ctg cga gtc cag cag ctg gtg caa gac ctg aag aaa ctg acc tgc      581
Leu Arg Val Gln Gln Leu Val Gln Asp Leu Lys Lys Leu Thr Cys
105         110         115
ag gtg gct act ctc aac aac aat ggt gag gaa gcc tcc act gaa ggg      629
ln Val Ala Thr Leu Asn Asn Asn Gly Glu Glu Ala Ser Thr Glu Gly
20          125         130         135
cc tgc tgc ccc gtc aac tgg gtg gag cac caa gac agc tgc tac tgg      677
hr Cys Cys Pro Val Asn Trp Val Glu His Gln Asp Ser Cys Tyr Trp
140         145         150

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ttc tct cac tct ggg atg tcc tgg gcc gag gct gag aag tac tgc cag Phe Ser His Ser Gly Met Ser Trp Ala Glu Ala Glu Lys Tyr Cys Gln 155 160 165	773
ctg aag aac gcc cac ctg gtg gtc atc aac tcc agg gag gag cag aat Leu Lys Asn Ala His Leu Val Val Ile Asn Ser Arg Glu Glu Gln Asn 170 175 180	821
ttt gtc cag aaa tat cta ggc tcc gca tac acc tgg atg ggc ctc agt Phe Val Gln Lys Tyr Leu Gly Ser Ala Tyr Thr Trp Met Gly Leu Ser 185 190 195	869
gac cct gaa gga gcc tgg aag tgg gtg gat gga aca gac tat gcg acc Asp Pro Glu Gly Ala Trp Lys Trp Val Asp Gly Thr Asp Tyr Ala Thr 200 205 210 215	917
ggc ttc cag aac tgg aag cca ggc cag cca gac gac tgg cag ggg cac Gly Phe Gln Asn Trp Lys Pro Gly Gln Pro Asp Asp Trp Gln Gly His 220 225 230	965
ggg ctg ggt gga ggc gag gac tgt gct cac ttc cat cca gac ggc agg Gly Leu Gly Gly Glu Asp Cys Ala His Phe His Pro Asp Gly Arg 235 240 245	1013
tgg aat gac gac gtc tgc cag agg ccc tac cac tgg gtc tgc gag gct Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr His Trp Val Cys Glu Ala 250 255 260	1061
ggc ctg ggt cag acc agc cag gag agt cac tgagctgcct ttgggtggac Gly Leu Gly Gln Thr Ser Gln Glu Ser His 265 270	1111
cacccggcca cagaaatggc ggtgggagga ggactcttct cacgacccctcc tcgcaagacc gctctggag agaaaataagc actgggagat tggaaagcact gctaacattt tgaatttttt tctcttaat tttaaaaaga tggatatgtg ttcttaagct tttatTTTT ttccaacttt tgaaaagtcaa cttcatgaag gtataatTTT tacataataa aaatgcactc atttaaagag aaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1370	1171 1231 1291 1351

<210> 10
<211> 273
<212> PRT
<213> Unknown

<220>
<223> mammalian nucleic acid and protein

<400> 10

Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys 1 5 10 15
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Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Leu 20 25 30

Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys Phe Gln Arg
 35 40 45

Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr Ser Asn Thr
 50 55 60

Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser Leu Glu Glu
 65 70 75 80

Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys Gln Glu Arg
 85 90 95

Gln Ala Val His Ser Glu Met Leu Leu Arg Val Gln Gln Leu Val Gln
 100 105 110

Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn Asn Asn Gly
 115 120 125

Glu Glu Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu
 130 135 140

His Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala
 145 150 155 160

Glu Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile
 165 170 175

Asn Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala
 180 185 190

Tyr Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val
 195 200 205

Asp Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln
 210 215 220

Pro Asp Asp Trp Gln Gly His Gly Leu Gly Gly Glu Asp Cys Ala
 225 230 235 240

His Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro
 245 250 255

Tyr His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser
 260 265 270

His

<210> 11
<211> 75
<212> PRT
<213> Unknown

<220>
<223> mammalian protein

<400> 11

Glu Lys Met Ile Ile Lys Glu Leu Asn Tyr Thr Glu Leu Glu Cys Thr
1 5 10 15

Lys Trp Ala Ser Leu Leu Glu Asp Lys Val Trp Ser Cys Cys Pro Lys
20 25 30

Asp Trp Lys Pro Phe Gly Ser Tyr Cys Tyr Phe Thr Ser Thr Asp Leu
35 40 45

Val Ala Ser Trp Asn Glu Ser Lys Glu Asn Cys Phe His Met Gly Ala
50 55 60

His Leu Val Val Ile His Ser Gln Glu Glu Gln
65 70 75

<210> 12
<211> 292
<212> PRT
<213> Unknown

<220>
<223> mammalian protein (ASGPR_m is a macrophage derived ASGPR)

<400> 12

Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys
1 5 10 15

Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln
20 25 30

Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly
35 40 45

Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys
50 55 60

Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr
 65 70 75 80

Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser
 85 90 95

Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys
 100 105 110

Gln Glu Arg Gln Ala Val His Ser Glu Met Leu Leu Arg Val Gln Gln
 115 120 125

Leu Val Gln Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn
 130 135 140

Asn Asn Gly Glu Glu Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn
 145 150 155 160

Trp Val Glu His Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met
 165 170 175

Ser Trp Ala Glu Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu
 180 185 190

Val Val Ile Asn Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu
 195 200 205

Gly Ser Ala Tyr Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp
 210 215 220

Lys Trp Val Asp Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys
 225 230 235 240

Pro Gly Gln Pro Asp Asp Trp Gln Gly His Gly Leu Gly Gly Glu
 245 250 255

Asp Cys Ala His Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys
 260 265 270

Gln Arg Pro Tyr His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser
 275 280 285

Gln Glu Ser His
 290

<210> 13
<211> 289
<212> PRT
<213> Unknown

<220>
<223> mammalian protein (DCMP2 short form)

<400> 13

Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys
1 5 10 15

Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln
20 25 30

Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly
35 40 45

Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys
50 55 60

Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr
65 70 75 80

Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser
85 90 95

Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys
100 105 110

Gln Glu Arg Gln Ala Val His Ser Glu Met Leu Leu Arg Val Gln Gln
115 120 125

Leu Val Gln Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn
130 135 140

Asn Asn Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu
145 150 155 160

His Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala
165 170 175

Glu Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile
180 185 190

20

Asn Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala
195 200 205

Tyr Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val
210 215 220

Asp Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln
225 230 235 240

Pro Asp Asn Trp Gln Gly His Gly Leu Gly Gly Glu Asp Cys Ala
245 250 255

His Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro
260 265 270

Tyr His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser
275 280 285

His